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September 15, 2004, 21:25:56; Search time 6853 Seconds (without alignments) 6830.655 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

PAT 17-JUL-2003

linear

DNA

1080 pb

Human glycosylation enzymes. BD270235

BD270235

RESULT 1 BD270235 LOCUS BD270235.1 GI:33080003 JP 2002537796-A/2. Homo sapiens (human) Homo sapiens

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 1080)

Coleman, T.A. and Betenbaugh, M.J.

Human glycosylation enzymes

Patent: JP 2002537796-A 2 12-NOV-2002;

REFERENCE AUTHORS TITLE JOURNAL

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	Match	Match Length	DB	ID	
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c 21	338	31.4	229321		AC094185	
	280.6	26.0	404		AX201885	
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24	269	25.0	201300	6	AL137073	uman 1
25	241	22.4	227816		AL683884	Mouse
56	241	•	244134		AC097073	AC097073 Rattus no
	7	•	1194		AF397531	AF397531 Drosophil
c 28	210	•	1999		AK123739	AK123739 Homo sapi
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	_	•	182381		AC122081	
c 31	Η,	•	191841		AC112827	Rattus
	-	•	266461		AC120718	
33	145.	13.5	292100		SC0939121	
	144	•	11237		AE012850	0
32	-		302300		AP005034	034
	126	•	298050		BX321861	
c 37			349652		BX569690	Synechoc
38	119.		15267		AB055099	Drosophi
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43	119.	ä	61		AC007594	007594
44	11	11.1	26		E003	36980
c 45	111.	10.4	æ		RCU57682	U57682 Rhodobacter

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Homo sapiens N-acetylneuraminic acid phosphate synthase mRNA,
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
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Cloning and expression of the human N-acetylneuraminic acid phosphate synthase gene with 2-keto-3-deoxy-D-glycero-D-galacto-nonnic acid biosynthetic ability
J. Boll Chem. 275 (23), 17869-17877 (2000)
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Lawrence, S.M., Huddleston, K.A., Pitts, L.R., Nguyen, N., Lee, Y.C.,
Vann, W.F., Coleman, T.A. and Betenbaugh, M.J.
Direct Submission
Submitted (18-APR-2000) Chemical Engineering, Johns Hopkins
 ATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCCAAGGTGTTGGAACGTCACATAACT
                                                                                                                                               TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCCTCGCTGGAGCCTGGAGAACTGGCC
                                                                                                                                                                                                 841 CIGCCIGIGAGAIGGCCIGCAAIGAGAAGCIGGGCAAGICIGIGGGGGCCAAAGIGAAA
                                                                                                                             TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCCTCGCTGGAGCCTGGAACTGGCC
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biosynthetic ability"
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/nol_type="mRNN"
/db_xref="taxon:9606"
/tisue_type="liver"
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02-MAR-1999 US 60/122409
TIMOTHY A COLEMAN,MICHAEL J BETENBAUGH
C12N15/09,A61K31/711,A61K38/43,A61K48/00,A61P1/02,A61P3/00, PC
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Location/Qualifiers
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Gl2N5/00,A61K37/48
Human glycosylation enzymes
                  Homo sapiens (huma
JP 2002537796-A/2
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Best Local Similarity 100.
Matches 1080; Conservative
                                                 12-NOV-2002
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ECGADCAKFOKSELEFKENRKALERPYTSKHSWGKTYGEHKRHLEFSHDOYRELORVA EEVGIFFTASGMDEMAVEFLHELNVPFYLGEHKRHLEFSHDOYRELORVA EEVGIFFTASGMDEMAVEFLHELNVPFYLGEDTUNFPYLEKTAKKGRPWVISSGMO SMDTMKQVYQIVKPLNPRNFFLQCTSAFLQPEDVIRKISEYGKLFPDIEIGYSGHE TGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLEFGELAELVRSVRLVERALGSP TKQLLPCEMACNEKLGKSVVAKVKIPEGTILITMDMLTVKVGEPKAYPPEDIFNLVGKK VLVTVEEDDTIMEELVDNHGKKIKS" Query Match Query Match Best Local Similarity 100.0%; Pred. No. 2.2e-256; Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1

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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bondldo, M.F., Casavant, F.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuti, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morernan, K.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lux, Gibbs, R.A.,
Fahey, J., Halton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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Homo sapiens N-acetylneuraminic acid synthase (sialic acid
synthase), mRNA (cDNA clone MGC:934 IMAGE:3505324), complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1229)
          CCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGTCTGTGGTGGCCCAAAGTGAAA
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                                                                                                                                                                                                                  TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC
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GCGADCAKFGKBELEFKFRKALDFYTSKHGWGRYYGEHRWRTHLEFSHDQYBELGRYA
EEUGIPFTAGGWBEAVFFLHELINVPFFKVGGGDTNNFPYLEKTAKKGRPWIISSGWD
SMDTMKQVYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIPIGYSGHP
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TKQLLPCEMACNBELGSSVVARVKIFBGTILTMDMLTVKVGGEPKGYPPEDIFULVGKK
VLVTVBEDDTIMBELVDNHGKKIKS"
Clone distribution: MGC clone distribution information can be round through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 9 Row: d Column. 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12056472. Location/Qualifiers
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/db_xref="CDD:COG2089"
                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="N-acetylneuraminic acid phosphate synthase"
/protein id="AAH19315.1"
/db_xref="G1:17939512"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATTGCCGAGATCGGCCGAGAACCAGCGAGGGCGACCTGGACGTAGCCAAGCGCATGATC
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                                                                                                                                               /organism="Homo sapiens"
//organism="mRNA"
//db xref="taxon:9606"
//clone="MGC:4339 IMAGE:2821389"
//clone="MGC:4339 IMAGE:2821389"
//clone Tib="MIH MGC 7"
//lone Tib="MIH MGC 7"
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Pred. No. 1.4e-255;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                           /note="synonym: SAS"
/db_xref="LocusID:54187"
/db_xref="MIM:605202"
                                                                                                                                                                                                                                                                                              'note="Vector: pOTB7"
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ECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKTYGEHKRHLEFSHDQYRELQRYA
EBVGIFFTASGMDEMAVBFLHELNVPFFKVGSGDTNNFPYLEKTAKKGRPMVISSGMQ
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TGIAI SVAAVALGAKVLERHI TLDKTWKGSDHSASLEPGELAELVRSVRLVERALGSP
TKQLLPCEMACNEKLGKSVVAKVKI PEGTI LTMDMLTVKVGEPKGYPPEDI FNLVGKK
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12056472.
Location/Qualifiers
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Direct Submission
Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Submitted (03-NOV-2000) National Institutes Office, National Cancer
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                              USA
NI H-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12652538.
Contact: MGC help desk
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/mol_type="mRNA"

/db_xref="teaxon:9606"

/clone="MGC:934 IMAGE:3505324"

/tissue_type="Placenta, choriocarcinoma"

/clone_lib="NHA MGC 21"

/lab_host="DH10B=R"

/note="Vector: pOTB7"
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/protein_id="AAH00008.1"
/db_xref="GI:12652539"
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biogenesis, outer membrane]"
/db xref="CDD:COG2089"
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/db_xref="LocusID:54187"
/db_xref="MIM:605202"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMAISU,
KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                           C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                                         Homo sapiens (human)
JP 2002191363-A/11392
09-JUL-2002
09-JUL-2000
28-JUL-2000
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                                                    C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
     Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Haten : JP 2002191363-4 11392 09-JUL-2002; HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11392
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAOI PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMM REIICHI NAGAI,TETSUJI OTSUKI
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1170)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
                                      TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG 300
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Primer for synthesizing full-length cDNA and use thereof.
BD156549
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JP 2002191363-A/11392.
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ENGTREYGOTVKPLANPROFTLQCTSAYPLQPEDVNLRVISEYGKLFPDIPIGYSGHE
TGIAISVAAVALGTKVLERHITLDKTWKGSDHSASLEPGELAELVRSVRLVERALGSP
TKQLLPCEMACNBEKGKSYVARVKIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKK
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AR001659 I GI:7023052 oligo capping, fis (full insert sequence). Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO buman cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; CDNA library construction, 5' a 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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Catarrhini; Hominidae; Homo.
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Unpublished
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Mammalia, Eutheria, Primates;
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[Bogai, T. and Otsuki, T. Direct Submission
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/mol_type="mrw"
/strain="129, G57BL/6J.FVB/N"
/db_xref="taxon:10000"
/clone="MGC:6592 IMAGE:3154822"
/tissue_type="Mammary tumor. Brcal-/fl; MMTV-Cre model. 10
months old, gross tissue."
/clone_lib="NCI_GAP_Mam3"
/lab_host="DHOB"
/note="Vector: pCMV-SPORT6"
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QEIGIFFTASGMDEMAVEFLHELNVPFFKVGSGDTNNFPYLEKTAKKGRPMVISSGMQ
SMDTMKQVYQIVKPLNPNFCFLQCTSAYPLQPEDANLRVISEYQKLFPDIPIGYSGHE
                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: 1 Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16716466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAH03307.1"
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|Ab_xref="Locus1D:94181"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLEPGELAELVRSVRLVERALGSP
TKQLLPCEMACNEKLGKSVVAKVKIPAGTTLTLDMLTVKVGEPKGYPPEDIFNLAGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATCATTGCCGAGATCGGCCAGAACCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 Argecerresaacresacresacresecercesecresaresarasacacceseres 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ATCATCGCGGAGATCGGCCAGAACCACCAAGGAGACATAGATGTGGCCAAGCGCATGATC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="SpsE; Region: Sialic acid synthase [Cell envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="N-acetylneuraminic acid synthase (sialic acid
       Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CGCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAGTITAATCGGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG
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Pred. No. 1.2e-207;
0; Mismatches 123; Indels
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/db_xref="CDD:COG2089"
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                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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957; Conservative
                                  Kowis, C.R., Snee
A.N., Gibbs, R.A.
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Haieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, Wh.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Munny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                         1031 GCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCCAAGAAGGTCCTGGTCACTGTTGAA
                                                                                                                                                 GCCTATCCTCTGAAGACATCTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA
                                               CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGTCTGTGGTGGCCAAAGTGAAA
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng I
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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/brotein_id="AAH57977.1"
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TKQLLPCEMACNEKGKSVVARVKIRAGSDFRANLRVKVGEPKGYPPEDIFNLAGKK
VLVTIEEDDTVMEESVESHSKKIKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 123 Row: f Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16716466. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearsson,R., Stantinpop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Douffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Scheil, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (108-582-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="N-acetylneuraminic acid synthase (sialic acid
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//clone lib="NCI CGAP_Li9"
//lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapBbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base; 1 to 1916)

Strauberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul; S.F., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haish, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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                  TTCCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGGATCTGGAGACACTAATAATTTT
                                                    TTTCTGCACGAACTGAATGTTCCCTTTTTCAAAGTTGGATCTGGGGACACTAACAATTTT
                                                                                                                                                                                                                                                      TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGC
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2 (bases 1 to 1174)
Kitajima, K. and Nakata, D.
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/codon_start=1
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ilarity 88.5%;
Conservative
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Pred. No. 1.2e-207;
0; Mismatches 123; ]
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26. .1057
/note="spsE; Region: Sialic abiogenesis, outer membrane]"
/db_xref="CDD:COG2089"
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Best Local Similarity 88.6
Matches 957; Conservative
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ECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKTYGEHKRHLEFSHDQYKELQSYA
OBIGIFFTASCHDEMAVEFLHELNVPPFKVGGGDTNNFPYLEKTAKKRPRMYISSGMQ
SMDIMKQVYQIVYDLNPFVFCLQCTSAYPLQPEDANLRVISETYGKLFDIFIGYSGHE
TGIALSVAAVALGAKVLERHTLLDKTWKGSDHSASLEPGELAELVRSVRLVBRALGSF
TKQLLPCEMACNEKLGKSVVAKCKIPAGTTLTLDTLTVKVGEPKGYPPEDIFINLAGKK
VLVTIBEDDTVMEESVESHSKKIKA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/protein id="BAA98131.1"
/db xref="GI:8978234"
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1 (Sites)

Nakata,D., Close,B.E., Colley,K.J., Matsuda,T. and Kitajima,K.

Molecular cloning and expression of the mouse N-acetylneuraminic
acid 9-phosphate synthase which does not have deaminoneuraminic
acid (Sin) 9-phosphate synthase activity

Blochem. Blophys. Res. Commun. 273 (2), 642-648 (2000)
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                            965 GGCTATCCTCCTGAAGACATCTTCAACCTAGGGGGAAAAAGGTGCTGGTCACTATCGAA
                                                                                                                              1025 GAAGATGACACGGTCATGGAAGAATCCGTGGAAAAGTCACAGCAAGAAAATCAAGGCTTAA
GCCTATCCTCCTGAAGACATCTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA
                                                                                                     GAGGATGACACCATCATGGAAGAATTGGTAGATAATCATGGCAAAAAAATCAAGTCTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-APR-2000) Ken Kitajima, Graduate school of bloagricultural sciences, Nagoya University, Department of ay Molecular biosciences; Chikusa-ku Hurou-chou, Nagoya, Aichi 464-8601, Japan (E-mail:kitajima@agr.nagoya-u.ac.jp, Tel:+81-52-789-4130, Fax:+81-52-789-4128)
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Pred. No. 2.9e-207;
0; Mismatches 124;
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/cell_line="COMMAld"
71. .1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1	Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB; HRI, and Biotechnology Center, National Institute of Technology and Evaluation; Clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. FEATURES Location/Qualifiers Source Location/Qualifiers	1 type="mkNa" capture	Matches 733; Conservative 0; Mismatches 1; Indels 0; Gaps 347 AGAIGGCAGTIGAATTCCTGCATGAATGTTCCATTTTTCAAAGTTGGATCTGGAG 2273 AGAIGGCAGTTGAATTCCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGGATCTGGAG 407 ACACTAATAATTTCCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGTCT 71	0y 467 CCACTGGGATGCAGTCAATGAACCAAGAAGTTTATCAGATGCCCTCA 526	2513 ACCTGCGGGTCATCTCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTG 647 GGCATGAAACAGCATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCCAAGGTTTCTG 618	QY 707 AACGTCACATAACTTTGGACAAGGACTGAAGGGAGTGACCACTGGCCTGGTGGAGC 766
181 AAGTTTAATCGGAAAGCCTTGGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG 181	431 421 491 481 551 541				OY 1021 GAGGATGACACCATCATGGAAGAATTGGTACATAATCAGGAAAAAAATCAGTTAA 1080	DEFINITION Homo sapiens CDNA FLJ33865 fis, clone CTONG2006515, highly similar to N-acetylneuraminic acid phosphate synthase. ACCESSION AK091184.1 GI:21749493 VERSION AK091184.1 GI:21749493 VERSION AK091184.1 GI:21749493 VERSION AK091184.1 GI:21749493 ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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PAT 17-JAN-2003
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Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 3682 09-JUL-2002;
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KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C C12P21/02,C12Q1/68/C12P21/08,G06P17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 813)

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TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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        TCAATGGACACCATGAAGCAAGTTTATCAGATGTGAAGCCCCTCAACCCCCAACTTTTGC
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                                                                        CCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG
                                                                                                                  TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGC
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Primer for synthesizing full-length cDNA and use thereof
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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JP 2002191363-A/3682
09-JUL-2002
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JP 2002191363-A/3682.
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                                                                                                                                                                      1007 TGGTCACTGTTGAAGAGGATGACCATCATGGAAGAATTGGTAGATAATGATGGCAAAA 1066
                                                                                                                                                                                        Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishi,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 3682 07-FEB-2001; Research Association for Biotechnology (JP)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
2813 TGGCCAAAGTGAAAATTCCGGAAGGCACCATTCTAACAATGGACATGCTCACGTGAAGG
                                                TGGCCAAAGTGAAAATTCCGGAAGGCACCATTCTAACAATGGACATGCTCACCGTGAAGG
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    .813
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                                                                           <u> ACCTGCGGGTCATCTCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTG</u>
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                                     Score 483.8; DB 6;
Pred. No. 8.6e-109;
0; Mismatches 9;
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    /db xref="taxon:9606"
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ilarity 98.2%;
Conservative 0
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Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesising full-length cDNA and their use
Patent: EP 1074617-A 8711 07-FEB-2001;
Research Association for Biotechnology (JP)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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(c) 1993 - 2004 Compugen Ltd.
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Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

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ALIGNMENTS

Human; glycosylation enzyme; glycolysis; myoglobinuria; tumour marker; immunotherapy; cosmetic surgery; metabolism; immune system disorder; haematopoietic cell deficiency; blood coagulation disorder; asthma; afibrinogenaemia; blood platelet disorder; thrombocytopaenia; neoplasia; autoimmune disorder; Addison's disease; multiple sclerosis; purpura; allergic encephalomyelitis; allergic reaction; organ rejection; graft-versus-host disease; inflammation; hyperproliferative disorder; sarcoidosis; infection; gene therapy; CMP sialic acid synthetase; ds. Human glycosylation enzyme clone HASAA37 coding sequence. AAA37763 standard; DNA; 1080 BP. (first entry) 04-DEC-2000 AAA37763; RESULT 1 AAA37763 A CHARLES ON THE STATE OF THE S

Homo sapiens

/product= "Sialic_acid_synthetase" Location/Qualifiers 1. .1080

WO200052136-A2

08-SEP-2000

01-MAR-2000; 2000WO-US005325

99US-0122409P 02-MAR-1999;

(HUMA-) HUMAN GENOME SCI INC.

Coleman TA;

WPI; 2000-572179/53. P-PSDB; AAY90352.

New human glycosylation enzymes cytidine 5'-monophosphate sialic acid synthetase, sialic acid synthetase and aldolase and nucleic acids encoding the proteins for treating e.g., immune system disorders, microbial diseases.

ABL29095

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Betenbaugh MJ,
Jarvis D;
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                                                 This sequence encodes a human glycosylation enzyme clone of the invention, designated HASAA37. The protein of this clone is a stalic acid synthetase. The sequences are useful as reagents for the differential identification of the tissues or call types present in a biological sample, as immunological probes, for treating a disease or condition resulting from under expression of such polypeptide, for the detection and/or treatment of disorders involving aberrant glycolysis, e.g. cramps, myoglobinuria, and as tumour marker and/or immunotherapy targets They may also be used to differentiate, proliferate and attract cells leading to the regeneration of tissues, to modulate mammalian characteristics to the regeneration of tissues, to modulate mammalian characteristics or anabolism processing, utilisation and energy storage, to change a manmal's mental state by influencing and as a food additive or sample, as a marker or detector of an immune system disorder, to inhibit cyckine activity, and as a vaccine. They may further be used to treat immune system or of haematopoietic cell deficiencies or disorders, blood coagulation disorders (e.g. thrombocytopaenia), wounds resulting from trauma or surgery, and an autoimmune or surgery, and an autoimmune disorders (e.g. thrombocytopaenia), wounds resulting from trauma or surgery, and an action of a sething or an autoimmune or surgery.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1080; Conservative 0; Mismatches
4; Page 110-111; 115pp; English
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/product= "sialic acid synthetase"
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(UYJO) UNIV JOHNS HOPKINS.
(UTEM) UNIV TEMPLE.
(UYWY-) UNIV WYOMING.
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/product= "Human SA synthetase protein"
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25-AUG-2000; 2000US-0227579P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for manipulating carbohydrate processing pathways in cells of interest. The methods are used to manipulate multiple pathways involved with the sialylation reaction by using recombinant DNA technology and substrate feeding approaches to using recombinant DNA technology and substrate feeding approaches to sialylation of sialylated glycoproteins in the cells. The combinate the production of sialylated glycoproteins in the cells. The sialylation process involves the post-translational addition of the donor cubbrate cytidine monophosphate-sialic acid (GMP-SA) onto a specific acceptor carbohydrate. The cells express at least one enzyme, selected complex synthetase and GMP-SA transporter, above endogenous levels. The cells are useful for producing complex sialylated glycoproteins in cells of interest, especially insect cells. Glycoproteins containing sialylated clls are useful as vaccines, therapeutics and diagnostic colls scand diagnostic consistence in the value of heterologous expression systems are useful for application of heterologous cell expression products as vaccines, therapeutics and diagnostic characeutics and diagnostic colls as well as increasing the variety of the heterologous proteins that can be produced and lowering biotechnology contenses, which is used in the method of the invention
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Matches 1080; Conservative
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GAGGATGACACCATCATGGAAGAATTGGTAGATAATCATGGCAAAAAAATCAAGTCTTAA
                                                                                                                CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCCAAGTCTGTGGTGGCCAAAGTGAAA
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                                                                                   ATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACT
                                                                                                                                                                                      TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCCTGGAGGAGCTGGAACTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sialic acid synthetase; human; sas gene; sialylation; glycoprotein; plasminogen; transferrin; thyrotropin; Na+,K+-ATPase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŢĀ;
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99US-0169624P.
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(UYJO) UNIV JOHNS HOPKINS.
(UYWY-) UNIV WYOMING.
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P-PSDB; AAY96101.
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                                                                                                                                                                Manipulating glycoprotein production in insect cell, involves enhancing expression of enzymes involved in carbohydrate processing pathway such as N-acetylglucosamine-2 epimerase or sialic acid synthetase.
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                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for manipulating glycoprotein production in an insect cell comprising enhancing expression of an cargyme, such as N acetylglucosamine-2 (GLNAc-2) epimerase, one catalysing conversion of UDP-GLONAc to mannose (Man) NAc, sialic acid synthetase, aldolase, cytidine monophosphate-sialic acid (CMP-SA) synthetase or CMP-SA transporter, where the expression of each enzyme is enhanced to above endogenous levels. The novel method is useful for manipulating glycoprotein production in an insect cell. Further methods of the invention are useful for producing slalylated glycoprotein. The useful as pharmaceutical compositions, vaccines, diagnostics and therapeutics. This polynucleotide sequence represents the DNA encoding a human SA synthetase protein of the invention
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The present sequence is unactor in uniqual count encouring stailed actor synthetase (see AAY96101), an enzyme that condenses ManNac-6-P or Man-6-P with PEP to form NeuSac and KDN phosphates, respectively. This novel complete termed SaS, was identified on the basis of homology with the scherichia coli neud gene using a bioinformatics based approach.

C Encherichia coli neud gene using a bioinformatics based approach.

Northern blots indicated ubiquitous transcription of the human synthetase compinantly engineered cells for producing plycoproteins having sialylated oligosaccharides. The methods involve altering the expression of enzymes involved in carbohydrate processing. A claimed cell producing sialylated glycoproferia at above endogenous levels expresses at least 1 (preferably human) enzyme selected from GLONAc-2 epimerase, an enzyme synthetase, andolase, CMP-sialic acid synthetase and adolase, CMP-sialic acid synthetase and cMP-sialic acid cransporter at above endogenous levels. Endogenous N-acetylglucosaminidase activity may be suppressed. A claimed method for acetylglucosaminidase activity may be suppressed. A claimed method for expression of 1 of the above enzymes, and a claimed method for sialylated glycoproteins involves expressing a heterologous protein cepper call by plasminogen, transferrin, Na+ K+-ATPase or thyrotropin) in the insect cell. Yeast, insect, fungal, plant and bacterial host cells can be engineered to produce new forms of sialylated glycoproteins and/or elevated concentrations of donor substrates (e.g. nucleotide sugars) required for eighter concentrations of donor substrates
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                                           sequence is that of human cDNA encoding sialic acid
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Disclosure; Page 103-105; 144pp; English
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Claim 4; SEQ ID NO 1192; 2081pp + Sequence Listing; English (HUMA-) HUMAN GENOME WPI; 2002-122018/16. P-PSDB; ABB90221. 40200190304-A2 Homo sapiens 24-MAY-2002 8 646 904 994 886 901 disorders, 601 199 721 781 841 961 1006 1021 1066 ABL90630; Birse RESULT 5 ABL90630 g ò g g ð g 유 d 8 ò ò ò g à 165 180 240 360 009 645 480 525 540 585 CCTTATCTGGAAAAAGCCCAAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCCAACTTCTGC TTCTTGCAGTGTACCAGCGCATACCCGCTCCAGCCTGAGGACGTCAACCTGCGGGGTCATC TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCCAACTTCTGC 991 481 586 121

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1020 1065 1080 1125 705 720 765 780 825 840 885 900 945 960 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiallergory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss. ATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACT CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCCAAGTCTGTGGTGGCCCAAAGTGAAAA GCCTATCCTCCTGAAGACATCTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA GCCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA GAGGATGACACCATCATGGAAGAATTGGTAGATAATCATGGCAAAAAATCAAGTCTTAA TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC ATAGCGATATCTGTGGCCCGCAGTGGCTCTGGGGGCCCAAGGTGTTGGAACGTCACATAACT TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCCTCGCTGGAGCCTGGAGAACTGGCC TIGGACAAGACCIGGAAGGGGAGIGACCACICGGCCICGCIGGAGCCCIGGACCIGGCC CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGTCTGTGGTGGCCAAAGTGAAA Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative Human polynucleotide SEQ ID NO 1192. ABL90630 standard; cDNA; 1268 18-MAY-2001; 2001WO-US016450 19-MAY-2000; 2000US-0205515P (first entry)

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      The invention relates to novel genes (ABL89449-ABL90853) and proteins candical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (art) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discrders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoardial ischaemias; (d) wound healing contections diseases such as wiral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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961 GCCTATCCTCCTGAAGACATCTTTAATCTAGTGGCAAGAAGGTCCTGGTCACTGTTGAA 1020 900 096 900 Q, treating disorders such Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; Ren F, Wang D; Zhang J, Zhao GGCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA Tregacaagaccregaagegeagreacacregecregeregagecregagaacregec CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGGCAAGTCTGTGGTGGCCAAAGTGAAA Qian XB, Yang Y, Novel nucleic acids and polypeptides, useful for as central nervous system injuries. Υ, ΑJ, Ma ΰ Chen R, Human polynucleotide SEQ ID NO 1345. man T, Xu (Drmanac RT; BP. 23-DEC-1999; 99US-00471275. 21-JAN-2000; 2000US-00488725. 25-APR-2000; 2000US-00552317. 20-JUN-2000; 2000US-00598042. 19-JUL-2000; 2000US-00598042. 03-AUG-2000; 2000US-00653450. 14-SEP-2000; 2000US-00665191. 19-OCT-2000; 2000US-00693036. 29-NOV-2000; 2000US-00693036. AAI59142 standard; cDNA; 1230 Liu C, Asundi V, Wang Z, Wehrman T, 26-DEC-2000; 2000WO-US034263 (first entry) Goodrich R, 2001-442253/47. (HYSE-) HYSEQ INC. P-PSDB; AAM39986 WO200153312-A1 leukaemia; ss Homo sapiens. 22-OCT-2001 26-JUL-2001 841 901 1081 1021 901 1141 AAI59142; 781 841 721 ٦, Q, Tang Wang Zhou AMAIS 9142 AMAIS 9142

Claim 1; SEQ ID NO 1345; 10078pp; English.

us-10-759-277-3.rng

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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form.
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Pred. No. 6.2e-314;
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Matches 1078; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030104529.
                                                            GCCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA
                                      GCCTATCCTCCTGAAGACATCTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA
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25-APR-2000; 2000US-00552317.
19-JUL-2000; 2000US-00620312.
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Sequence 1170 BP; 294 A; 285 C; 347 G; 244 T; 0 U; 0 Other;
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The present invention describes primer sets for synthesising 5602 full-

(a) an oligo-dr primer and an oligomorlectide complementary to the

complementary strand of a polymuclectide comprises one of the 5602

complementary strand of a polymuclectide which comprises one of the 5602

complementary strand of a polymuclectide which comprises one of the 5602

complementary strand of a polymuclectides, or (b) a combination

of an oligomuclectide comprising a sequence complementary to the

complementary strand of a polymuclectide which comprises a 5'-end

sequence and an oligomuclectide comprising a sequence complementary to a

complementary strand of a polymuclectide which comprises a 5'-end

sequence and an oligomuclectide comprising a sequence complementary to a

complementary strand of a polymuclectide which complementary to a

complementary strand of a polymuclectide which complementary to a

complementary strand of a polymuclectide of sequence, where the

complementary strand of sequence is selected from those defined in the

configuration. The primer sets can be used in antisense therapy and in

complementary full-length cDNAs. The primers are also useful for the

complementary full-length cDNAs. The primers are also useful for the

configuration and/or diagnosis of the abnormality of the proteins encoded by

configuration without any specialised methods. AAH03166 to AAH13628

configuration of the main amino acid sequences; and AAH13629 to AAH13632 represent

coligomuclectides. all of which are used in the exemplification of the
Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ ID NO:12129
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                         standard; cDNA; 1170
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27-AUG-1999; 99JP-00300253.
17-AUG-1999; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cyrostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, municipen's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activin/inhibin activity, chemclactic/chemchinetic activity, haemostatic assays for receptor activity, arthritis and theraper.
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, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'el nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancerparipheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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Pred. No. 4.5e-260;
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Xue AJ,
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Irman T, Xu C, X
Drmanac RT;
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     BP.
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2000US-00620312.
2000US-00653450.
2000US-00662191.
2000US-00693036.
AAI60928 standard; cDNA; 1243
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Wehrman T,
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2000US-00488725.
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Best Local Similarity 89.6%;
Matches 1041; Conservative
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Wang Z, Wehr
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21-JAN-2000;
25-APR-2000;
20-JUN-2000;
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03-AUG-2000;
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Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Partkinson's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder; thrombosis; wound healing; ss.
                                                                                                                                                                          DNA encoding human secreted protein, Seq ID No 100
                         1209 TCACTGTTGAAGAGGATGACACCATCATGGAAGAA 1243
          1010 TCACTGTTGAAGAGGATGACACCATCATGGAAGAA
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2000US-0224518P.
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AAS33141 standard;
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26-JUL-2000;
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14-AUG-2000;
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02-MAR-2000;
16-MAR-2000;
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11-JUL-2000;
11-JUL-2000;
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18-AUG-2000;
22-AUG-2000;
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28-JUN-2000;
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                                        CGCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC
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The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, creat or ameliorate a medical condition in e.g. humans, mice, rabbits, creat or ameliorate a medical condition in e.g. humans, mice, rabbits, creat not adops, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary consequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be inneed of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted constitution of antibodies and antagonists may also be used as diagnostic agents for detecting the presence of (II) antibodies and activity of (II). The anti-(II) antibodies con may also be used as diagnostic agents for detecting the presence of (II) disorders include for example: immune/sorbant assay (ELISA)). The disorders include for example: immune/sorbant assay (ELISA)). The disorders include for example: immune/sorbant assay (ELISA). The anti-(II) antibodias and hyperproliferative disorders (e.g. Human immunodeficiency virus) infections, aneania, rheumatorid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
Gaucher's disease and Charcot-Marie-Tooth disease), cardio-/
Cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and cerebrand successions and subicons and subicons and subicons and subicons and subicons and support cell culture of primary tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions.
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17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251930P.
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P-PSDB; AAU20432.
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Query Match 67.8%; Score 732; DB 4; Length 1238; Best Local Similarity 99.7%; Pred. No. 6.5e-210; Matches 732; Conservative 1; Mismatches 1; Indels 0;

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TGGGTGAGCCCAAAGCCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCC 1006
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The present invention describes primer sets for synthesising 5602 full-

(a) an oligo-dr primer and an oligonaclectide complementary to the

complementary strand of a polynucleotide which comprises one of the 5602

complementary strand of a polynucleotide which comprises one of the 5602

complementary strand of a least 15 nucleotides; or (b) a combination

of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a forest complementary to a

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide of sequence, where the

complementary strand of a polynucleotide of sequence, where the

complementary strand of sequence is selected from those defined in the

conjugantication. The primer sets can be used in antisense therapy and in

specification. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

cut the full-length cDNAs. The primers are also useful for the

cut cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

AAH13633 to AAH13632 represent human cDNA sequences; AAB93446 to AAB95893

crepresent human amino acid sequences; and AAH13629 to AAH13632 represent

constant invention of the accompliance of the processent invention of the accompliance of the accomplementary and and are used in the exemplification of the
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                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCATTGCCGAGATCGGCCAGAACCACCAGGCGACCTGGACGTAGCCAAGCGCATGATC
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                                           Yamamoto J;
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Pred. No. 2e-203;
); Mismatches 8; Indels 2.
                                                                                                                                                                                                                                                                         SEQ ID NO 3682; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 813 BP; 198 A; 199 C; 243 G; 168 T; 0 U; 5 Other;
                                           Saito K,
Otsuki
                                           Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                       Wakamatsu
                                      sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
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(HELI-) HELIX RES INST.
                                                                                                              WPI; 2001-318749/34.
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Best Local Similarity
                                             Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention
                                             Ota T, IE
Ishii S,
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TTCCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGGATCTGGAGACACTAATAATTTT

311 TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG TACGCCGAGGAGGTTGGGATCTTCTTCACTGCCTCTGGCATGGATGAGATGCCAGTTGAA CCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG 480

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CCTTATCTGGAAAAGACAGNCAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprising a sequence.
                                             TTCTTGCAGTGTACCAGCGCATACCCGCTCCAGCCTGAGGACGTCAACCTGCGGGTCATC
                                                                                                      ATAGCGATATCTGTGGCCGCAGTGGC-TCTGGGGGCCAAGGTGTTGGAACGTCACATAAC
                                                                                                                                             CTITCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC
                                                                                                                                                                       TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC
                                                                                                                                                                                                                                ATAGCGATATCTGTGGCCGCAGTGGCTTTTGGGGACCAAGGTGNTGGAACGTCACAT-AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                              TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 8711; 2537pp + Sequence Listing; English.
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Otsuki
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA clone (3'-primer) SEQ ID NO:8711.
                                                                                                                                                                                                                                                                               TTTGGACAAGACCTGGAANGGGAG 813
                                                                                                                                                                                                                                                             TTTGGACAAGACCTGGAAGGGGAG 743
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11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                               AAH11876 standard; cDNA; 514
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oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence's relected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the primers are also useful for the the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are also useful for the AAH13613 to AAH13612 to AAH13628 and AAH13613 to AAH13612 represent human amino acid sequences, and AAH13629 to AAH13629 represent coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                 455
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                                                                                                                                                                                                                                                                                                                     514 ACNTGNGGGTNNTNTNGGAANATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTG
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                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                      Length 514;
                                                                                                                                                                                                    Sequence 514 BP; 112 A; 149 C; 113 G; 133 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #27641.
                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                    Score 483.8; DB 4;
Pred. No. 3.3e-135;
0; Mismatches 9;
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                                                                                                                                                                                                                                    44.88;
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                                                                                                                                                                        present invention
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ABN95016 standard; DNA; 464 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal genes. (I) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating polypeptide in tissue, as molecular weight markers and as a food superprine in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypuncleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and polypuncleotide sequences have applications on puny and proposed and polypup conterns of mutations and polypup content of markers and activity of the polypup content of mutations and polypup content of mutations and polypup content of mutations and polypup content content traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rcaaarcgrgaagccccrcaacccaacrrcrgcrrrrrgcagrgraccagcgcaracc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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2000US-00649167,
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                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, dung toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form bart of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                     Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
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AAGGTGGGTGAGCCCAAAGCCTATCCTCCTGAAGACATCTTTAATCTAGTGGCAAGAAG 1002
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                                                                                                                                                                                                                                                                                             Mitochondrial function, Forkhead Related Activator-2; FREAC-2; apoptosis; neurodegenerative disease; proliferative disorder; cancer; neurological disease, Alzheimer's disease; AD; multiple sclerosis; MS; Parkinson's disease; DD; vascular dementia; diffuse Lewy body disease; DDB; amylotrophic lateral sclerosis; ALS; MS; myoclonic epilepsy lactic acidosis and stroke; MELAS; MERRE; myoclonic epilepsy ragged red fibre syndrome; autoimmune disease; gene therapy; antisense therapy; ds.
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                                                                                                 464 TCTGGGCATGAAACAGGCATAAGCGATATCTGTGGCCGCAGTGGCTCTTGGGGCCAAGTTG
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                                                                          TCTGGGCATGAAACAGGCATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTG
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                                                       Gaps
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                          Score 418; DB 6; Length 464;
Pred. No. 2.2e-115;
0; Mismatches 5; Indels
  U; 0 Other;
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Sequence 464 BP; 101 A; 133 C; 103 G; 127 T; 0
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ilarity 98.6%;
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The invention describes a method of identifying an agent that alters a mitochondrial function, comprising inducing Forkhead Related Activator-2 (FREAC-2) expression in a host cell in the presence and absence of a candidate agent, and screening for an agent which alters the level of apoptosis resulting from such induced FREAC-2 expression. The method is useful for identifying an agent that alters a mitochondrial function, cepecially apoptosis. The invention also describes a method for treating continuation also describes a method for treating a molecular target for therapeutic intervention for treating invention are useful for treating a disease associated with inappropriate content invention are useful for treating a disease associated with inappropriate cell proliferation or cell survival, in particular cancer, or a neurological disease or disorder including Alahaimer's disease (AD), multiple sclerosis (MS), parkinson's disease (PD), diffuse Lewy body disease (DLB), vascular dementia, amylotrophic lateral sclerosis (ALS), contending cepilepsy lactic acidosis and stroke (MELAS), myoclonic epilepsy and also autoimmune diseases. This sequence represents a polynucleotide in the invention and also autoimmune diseases. This sequence represents a polynucleotide incomment of invention and also autoimmune diseases.
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Search completed: September 16, 2004, 02:09:58 Job time : 674 secs

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Sequence 3, Appli
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Sequence 1479, Ap
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Sequence 13238, A
Sequence 9674, Ap
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Sequence 13551, A
Sequence 13551, A
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Sequence 13787, A
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Sequence 12255, A
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Sequence 1, Appli
Sequence 15530, A
Sequence 15530, A
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-09-620-312D-1035
4 US-08-916-421B-1
4 US-08-976-25-81
4 US-09-495-406-1
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US-09-252-991A-15630

US-09-252-991A-15757

US-09-252-991A-15590

US-09-252-991A-15590
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Maximum Match 100%
Listing first 45 summaries
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US-09-252-991A-8364 US-09-252-991A-11427 US-09-669-751-140 US-09-552-991A-11391 US-09-252-991A-11391 US-09-310-181-3 US-09-930-181-3 US-09-930-181-3 US-09-930-181-3 US-09-930-181-3 US-09-103-840A-2 US-09-103-840A-1 US-09-103-840A-1 US-09-103-840A-1 US-09-252-991A-5919 US-09-252-991A-5968	ALIGNMENTS 19516143A 1ences, Inc. Glycosylation Enzymes US/09/516,143A 03-01 60/122,409	1080; DB 4; No. 1.3e-302; matches 0;		ATCATTGCCGAGATCGGCCAGAACCACAGGGCGACCTGGACGTAGCCAAGCGCATGATC 	CGCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC	aagittaatoggaaagcottggagaggocatacacotogaagcattootggggaagagg 	TACGGGGAGCACAAACGACTTCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG
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FILE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
FRIOR APPLICATION NUMBER: 09/552,317
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARKE: Pt_IL_Genes Version 1.0
SEQ ID NO 1035
LENGTH: 1230
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.8
Matches 1078, Conservative
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US-09-620-312D-1035
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Patent No. 6569662

GENERAL INPORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Man, Yunqing
APPLICANT: Man, Yunqing
APPLICANT: Wang, Dinrui
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APPLICANT: Wang, Dinrui
APPLICANT: Wang, Raindiast
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US-09-620-312D-1035
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or
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LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (191995)...(191995)
OTHER INFORMATION: nequals a, t, c, NAME/KEY: misc feature
LOCATION: (231980)...(231980)
OTHER INFORMATION: nequals a, t, c, NAME/KEY: misc feature
LOCATION: (234187)...(234187)
OTHER INFORMATION: nequals a, t, c, NAME/KEY: misc feature
LOCATION: (234187)...(234187)
OTHER INFORMATION: nequals a, t, c, NAME/KEY: misc feature
LOCATION: (234220)...(234220)
OTHER INFORMATION: nequals a, t, c, NAME/KEY: misc feature
LOCATION: (2343814)...(234814)
OTHER INFORMATION: nequals a, t, c, NAME/KEY: misc feature
LOCATION: (2343814)...(234814)
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LOCATION: (319226)...(319226)
OTHER INFORMATION: n equals a, t, c,
NAMEAKEY: misc feature
LOCATION: (559167)...(559167)
OTHER INFORMATION: n equals a, t, c,
NAMEAKEY: misc feature
LOCATION: (559241)...(559241)
OTHER INFORMATION: n equals a, t, c,
NAMEAKEY: misc feature
LOCATION: (600992)...(600992)
OTHER INFORMATION: n equals a, t, c,
NAMEAKEY: misc feature
LOCATION: (622708)...(62098)
OTHER INFORMATION: n equals a, t, c,
NAMEAKEY: misc feature
LOCATION: (622708)...(622708)
              NAME/KEY: misc feature
LOCATION: (103998). (103998)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (148948). (148948)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191599). (191989)
OTHER INFORMATION: n equals a, t,
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LOCATION: (657081)...(657081)
NAME/KEY: misc feature
LOCATION: (657203)...(657203)
OTHER INFORMATION: n equals a, t,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t,
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      OTHER INFORMATION: n equals a, t,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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OTHER INDEMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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839 TIGGACAAGACCIGGAAGGGGAGIGACCACICGGCCICGCIGGAGCCIGGAGAACIGGCC 898
                                                               899 GAGCTGGTGCGTCAGTGCGTCTTGTGGAGCGTGCCCTGGGCTCCCCAAGCAGCTG
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                                                                                                                   CTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCCAAGTGTGTGGTGGCCAAAGTGAAA
                                       FEATURE:
NAME/KEY: misc feature
LOCATION: (2822). (18322)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257). (18258)
OTHER INFORMATION: n equals a, t, c, or g
LOCATION: (84773). (84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84868). (84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84812). (84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84812). (84812)
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or
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OTHER INPORMATION: n equals a, t, c,
NAME/KEY: misc. feature
LOCATION: (98343)..(98343)
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 81, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-2540
INFORMATION FOR SEQ 1D NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 base pairs
TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
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US-08-976-259-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 CAATGGTGATCTCCAGTGGGATGCAGTCAAT---GGACACCATGAAGCAAGTTTATCAGA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 ATGACCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGGATCTTCACTGCCT
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Pred. No. 9.9e-10;
0; Mismatches 334;
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                                                                                                                                                       LOCATION: (871619).
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (1084830). (1084830)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
                                                            LOCATION: (779676) ... (779676)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc_feature
LOCATION: (855539) ... (855539)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
             LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                       ION: (1096846)..(1096846)
INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1602912)..(1602912)
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Best Local Similarity 46.9%;
Matches 300; Conservative
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465973 CTTATGAAGATGTCAATTTAAAGGCTATTAAAACCTTGAAAAGTATATTCAAT---ATCC 466029
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TCGTGAAGCCCCTCAACCCCCAACTTCTGCTTCTTGCAGTGTACCAGCGCATACCCGCTCC
                                                            465913 TAGAAATAATGGATGCAGGGATATTATTTTTTTTGCATTGTATTCATCTTACCCAACCC
                                                                                                                                                572 AGCCTGAGGACGTCAACCTGCGGGTCATCTCGGAATATCAGAAGCTCTTTCCTGACATTC
                                                                                                                                                                                                                                                                                                CCATAGGGTATTCTGGGCATGAAACAGGCATAGCGATATCTGTGGGCCGCAGTGGCTCTGG
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APPLICANT: Chol, Gil H.
APPLICANT: Walch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              872 TGGGCAAGTCTGTGGTGGCCAAAGTGAAATTCCGGAAGG 911
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ZIP: 2006-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPITER: HP Vectra 486/33
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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us-10-759-277-3.rni

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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ITLE OF INVENTION: AERUGINOSA FOR DIF
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US-09-252-991A-6241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE PEPERENCE: 019633-0001100sides and Ganglioside Mimics
                                                                                                                                                                                                                  122 GCATGGCCAAGGAGTGTGGGCCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTCA
                                                                                                                                  62 TCATTGCCGAGATCGGCCAGAACCACCAGGGCGACCTGGACGTAGCCCAAGCGCATGATCC
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                                                        Length 1234;
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OTHER INFORMATION: including LOS biosynthesis locus
                                                    4.9%; Score 52.6; DB 4; Length 1
48.5%; Pred. No. 2.9e-05;
iive 0; Mismatches 184; Indels
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CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09495406
Patent No. 6503744
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                                                Query Match
Best Local Similarity 48.5
Matches 179; Conservative
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.2
Matches 169; Conservative
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US-08-976-259-81
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6409
                                                                                                                                                                                                             7451 AATGCACAACCAATCTTTACCCAACCCCGCATAATCTTGTAAGATTAAACGCTATGCT 7510
                                                                                                                                                                                                                                                                                                                                                             7511 TGAATTAAAAAAGAATTTTCTTGTATGG----TAGGCTTAAGCGACCACACAACAGATAA 7567
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                                                                                                                                        543 CITGCAGTGTACCAGCGCATACCCGCTCCAGCCTGAGGACGTCAACCTGCGGGTCATCTC 602
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483 AATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGCTT
                                                                1391 TATTGAAAGTATAAAACCAACTGTAAAATCTTATTAGACAATGAAATTCCCTTTGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         663 AGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACT
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49.1%; Pred. No. 0.013;
tive 0; Mismatches 146; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6409, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6409
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DB 1; Length 7218;

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88 CAGGGCGACCTGGACGTAGCCAAGCGCATGATCCGCATGGCCAAGGAGTGTGGGGCTGAT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 CCATACACCTCGAAGCATTCCTGGGGGAAGACGTACGGGGGAGCACAAACGACATCTGGAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 TICAGCCATGACCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGATCTTCTTC 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 ITCAAAGTIGGATCTGGAGACACTAATAATTTTCCTTATCTGGAAAAGACAGCCAAAAAA 447
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                                                                                                                                                                                                                                                                                                                                                               18; Conservative 209; Mismatches 170;
  REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                       Score 41.4;
                                                                                                                                                                                                                                                                                                                                             Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1478, Application US/09833381
Patent No. 6672186
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) OTHER INFORMATION: n = A,T,C or

US-09-833-381-1478
               TELECOMMUNICATION INFORMATION
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                             TOPOLOGY: 1111....
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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LENGTH: 2437
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US-08-232-463-14
                                                                                                                                              LENGIH:
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                                                                                                                                                                                                                                                                                                   Score 43.4; DB 4; Length 1104;
Pred. No. 0.013;
0; Mismatches 146; Indels 3
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GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TILE OF INVENTION: RECOMBINANT FOWLEOX VIRUS
NUMBER OF SEQUENCES: 5.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
ZIP: Z2313-0299
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; SEQ ID NO 6241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,768
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.1%;
Matches 144; Conservative
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                                                                                                                                                                                             LENGTH: 1104
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APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-100 NUMBER: US/09/833,381
CURRENT APPLICATION NUMBER: US/09/833,381
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 20050
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8%; Score 41; DB 4; Length 2437;
1075 RRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAA 1039
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Sequence 9714, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc Of Rubenfield et al.
APPLICANT: Marc Of Rubenfield et al.
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9714
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 CGAAGCATTCCTGGGGGAAGACGTACGGGGAGCACAAACGACATCTGGAGTTCAGCCATG 277
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49.3%; Pred. No. 0.23;
tive 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match
3.7%; Score 40; DB 4; Length 738;
Best Local Similarity 55.9%; Pred. No. 0.1;
Matches 76; Conservative 0; Mismatches 60; Indels
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                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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                           SEQ ID NO 13238
                                                                                        LENGTH: 738
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUCINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                   1803 GCCAAGCGGCAGAAGGACCGCAAGGCCCATCGCCCGCTTCCAGCAGGGACAGCAGGAGGGGCGG 1862
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Fatent No. 6672186
GENERAL INFORMATION:
APPLICANT: RObison, Keith E.
TITLE OF INVENTION:
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT APPLICATION NUMBER: US/09/833,381
FILE REPERENCE: 5001-04-11
FRIOR APPLICATION NUMBER: 09/516,448
FRIOR PRIOR PARE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1479
                                                                                                                                                                     724 GACAAGACCTGGAAGGGGAGTGACCACTCGGCCTGGAGCCTGGAGAACTGGCCGAG
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Best Local Similarity 52.7%; Pred. No. 0.095;
Matches 89; Conservative 0; Mismatches 80; Indels
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OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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US-09-833-381-1479
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completed: September 16, 2004, 05:31:28
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Best Local Similarity 56.8'
Matches 67; Conservative
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US-09-252-991A-13452
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
SEQ ID NO 96 SEQ ID NOS: 33142
LENGTH: 1254
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49.3%; Pred. No. 0.43;
ive 0; Mismatches 103; Indels
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US-09-252-91A-9533/c
Sequence 9533, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-9533
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Best Local Similarity 49.33
Matches 100; Conservative
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US-09-252-991A-9674
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Best Local S.
Matches 100
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Sequence 13452. Application US/09252991A
Sequence 13452. Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13452
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56.8%; Pred. No. 0.89;
iive 0; Mismatches 51;
877 AAGTCTGTGGTGGCCAAAGTGAA 899
                                                                370 ATGACCGCGGAGTCCTACAAGAA 348
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61 ATCATTGCCGAGATCGCCAGAACCACCAGGCGACCTGGACGTAGCCAAGCGCATGATC 120
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Sequence 3, Appli
Sequence 1192, Ap
Sequence 1193, Ap
Sequence 1035, Ap
Sequence 1035, Ap
Sequence 2220, Ap
Sequence 2220, Ap
Sequence 2343, A
Sequence 2343, A
Sequence 1933, A
Sequence 1933, A
Sequence 1933, A
Sequence 1933, A
Sequence 1833, A
Sequence 1833, A
Sequence 1833, A
Sequence 1833, A
                                                                                                                                                                 September 16, 2004, 04:04:27; Search time 5258 Seconds (without alignments) 1036.752 Million cell updates/sec
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2: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

5: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

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7: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*

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7: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*

7: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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16 US-10-264-237-1192

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16 US-10-117-722-1035

17 US-09-980-107-1514

18 US-09-918-995-5220

18 US-09-918-995-5220

18 US-09-918-995-2343

18 US-09-918-995-1953

18 US-10-181-447A-18

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US-10-085-783A-31232
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Sequence 31232, A	Seguence 3360. Ap	Segmence 1 Appl	Sequence 83. Appl	Sequence 83. Appl	Seguence 1. Appli	Sequence 1941. Ap	Seguence 7, Appli	31		Sequence	907	Sequence 81, Appl	Sequence 25490. A	Sequence 5, Appli	H	~	· ~	Ä	Sequence 18, Appl	H	quence 1.	, , , (0	-	H	'n		Н	Sequence 1479. Ap	e 6436.	261	
6 US-10-242-535A-31232	5 US-10-156-761-3360	5 US-10-156-76	US-09-870-7	ns		ns	US-09-930-440B-	7 US-10-343-561-31	US-09-925-299-701		ns								3 US-10-321-396C-18				5 US-10-303-118-1	US-10-303-128	US-10-303-134		US-09-833-381-1478	US-09-833-381-1479	S US-10-156-761-6436	-91	
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	135	135	101.6	101.6	95.2	85	63	62.8	62	62	9	52.6	52.2	49.6	49.6	49.6	49.6	49.6	49.6	49.6	44.4	44.4	44.4	44.4	44.4	44.4	41	41	40.2		
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US-09-984-205-3

Sequence 3, Application US/09984205

Patent No. US20020137175A1

GENERAL INFORMATION:

APPLICANT: COleman, Timothy A. et al.

TITLE OF INVENTION: Human Glycosylation Enzymes

FILE REPRENCE: PF505D1

CURRENT APPLICATION NUMBER: US/09/984,205

CURRENT PILING DATE: 2001-10-29

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 69/516,143

PRIOR APPLICATION NUMBER: 69/516,143

PRIOR PRIOR APPLICATION NUMBER: 60/122,409

PRIOR FILING DATE: 1999-03-02

NUMBER OF SEQ ID NOS: 6

SOSTWARR: PATENTIN PATENTIN ON: 2.1
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ORGANISM: Homo sapiens
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; TITLE OF INVENTION: Engineering Intracellular Sis; FILE REFERENCE: PF509P2; CURRENT APPLICATION NUMBER: US/09/930,440B; CURRENT FILING DATE: 2001-08-16; PRIOR APPLICATION NUMBER: 60/227,579	FRIOR FILLING DATE: 2000-29-29-29-29-29-29-29-29-29-29-29-29-29-	FRIOR FILLING DAILS: 1939-12-09 FRIOR APPLICATION NUMBER: 60/122,582 FRIOR FILLING DATE: 1999-03-02 ; NUMBER OF SEQ ID NOS: 8	SEQ ID NO 5 LENGTH: 1080 TYPE: DNA 9		Query Match 100.0%; Score 1080; DB 9 Best Local Similarity 100.0%; Pred. No. 0; Marches 0	rererecedece	ΨΨ		181	2 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	301	361	421 421 6	481	DD 481 TCATGGAGTGTACCAGGCAAGTITATCAGATGGTGAAGCAGGCATACCCGGCTCCAGCCTGAGCATACCCAGCGCATACCCAGCCTGAGCATACCCAGCCTGAGCATACCCAGCATACCCAGCATACCAGCATACCAGCATACCAGCATACAGCATACAGCATACAGCATACAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	Db 541 Tretrecagnerachaedechracedecreehaedecreehaedecreehae
61 ATCATTGCCGAGATCGGCCAGAACCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATC 120 121 CGCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC 180 121 CGCATGGCCAAGGAGTGTGGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC 180 121 CGCATGGCCAAGGAGTGTGGGGGCTGATTGTGCCAAGTTCCAGAAGAGGAGTGAGAATTC 180	181 AAGITIAATCGGAAAGCCITGGAGAGGCCAFACACCTCGAAGCATTCCTGGGGGAAGACG 240 	241 TACGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG 300 241 TACGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG 300	301 TACGCCGAGGAGGTTGGGATCTTCACTGCCTCTGGCATGGATGAGGTGGCAGTTGAA 360 	361 TICCIGCAIGAACIGAAIGITCCAITITICAAAGIIGGAICIGGAGACACIAAIAAITIT 420 	421 CCTTATCTGGAAAAGACAGCCAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG 480 	481 TCAATGGACCCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGC 540	541 TICTIGCAGIGIACCAGCGCAIACCGGCTCCAGCCTGAGGACGTCAACCTGCGGGTCAIC 600 [601 TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC 660 	661 ATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGCCCAAGGTGTTGGAACGTCACATAACT 720 	721 TTGGACAAGACCTGGAAGAGGGGGGGGGGCTCGCTGGAGCCTGGAGAACTGGCC 780 	781 GAGCTGGTGCGGTCAGTGCGTCTTGTGGAGCGTGCCCTCGGCTCCCCAACCAA	841 CTGCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGTCTGTGGTGGCCAAAGTGAAA 900 	901 AITCCGGAAGGCACCATICTAACAAIGGACAIGCTCACCGIGAAGGTGGGTGACCCCAAA 960 	961 GCCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA 1020 	1021 GAGGATGACCATCATGGAAGAATTGGTAGATAATCATGGCAAAAAAATCAAGTCTTAA 1080 	1021 GAGGALGACACCALCATGGGAAGAALGGGGGGGGGGGGGG
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RESULT 2
US.09-30-440B-5
:Sequence 5, Application US/09930440B
; Patent No. US20020142386A1
; GENERAL INPORMATION:
; APPLICANT: Betenbaugh et al.

TTCGAAGCATTCCTGGGGGAAGAG 240 ATGGTGATCTCCAGTGGGATGCAG 480 SAAGCCCTCAACCCAACTTCTGC 540 009 661 ATAGCGATATCTGTGGCCCCGCAGTGGCTCTGGGGGCCCAAGGTGTTGGAACGTCACATAACT 720 TTCCAGAAGAGTGAGCTAGAATTC 180 GAGGACGTCAACCTGCGGGTCATC 600 GACCAGTACAGGGAGCTGCAGAGG 300 GGCATGGATGAGATGGCAGTTGAA 360 GGATCTGGAGACACTAATAATTT 420 CTGGACGTAGCCAAGCGCATGATC 120 CTGGACGTAGCCAAGCGCATGATC 120 GOTGGGGGGGGAACACCCGTGCTTC 60 Gaps ialylation Pathways . , 9; Length 1080; 0; Indels дq ò õ

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Sequence 1192, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAL311P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: US 60/205,515
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                                                                          CGCATGGCCAAGGAGTGTGGGCTGATTGTCCAAGTTCCAGAAGAGTGAGAGTTCCAGAATTC
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Publication No. US20040142442A1

GENERAL INFORMATION:

APPLICANT: Coleman, Timothy A. et al.

TILLE OF INVENTION: Human Glycosylation Enzymes

FILLE REFREENCE: PF505D1

CURRENT APPLICATION NUMBER: US/10/759,277

CURRENT FILING DATE: 2004-01-20

PRIOR APPLICATION NUMBER: US/09/984,205

PRIOR APPLICATION NUMBER: PCT/US00/05325

PRIOR APPLICATION NUMBER: PCT/US00/05325

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 1999-03-02

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 3

LENGTH: 1080
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; Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.0
Matches 1080; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)..(1077)
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APPLICANT: Tillinghast, John
APPLICANT: Drmansk, Gadoje T.
TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1035, Application US/10037270
Publication No. US20030104529A1
GENERAL INPORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jina-Rui
APPLICANT: Wang, Jina-Rui
APPLICANT: Wang, Jihwei
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US-10-037-270-1035
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99.8%; Pred. No. 0;
iive 1; Mismatches
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LOCATION: (1230)..(1230)
OTHER INFORMATION: n equals a,t,g, o)
FRATURE:
NAME/KEY: misc feature
LOCATION: (1257)..(1257)
OTHER INFORMATION: n equals a,t,g, o)
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NAME/KEY: misc_feature
LOCATION: (17)...(17)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (31)...(31)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                         DOCATION: (5)...(5)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                        a,t,g,
                                                                                                                                                                                                                                                                                                                                                                          a,t,g,
                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (27)...(27)
OTHER INFORMATION: n equals
PRIOR FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)...(23)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1224)..(1227)
OTHER INFORMATION: n equals
          NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 1192
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                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                               NAME/KEY: misc feature LOCATION: (5)..(5)
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NAME/KEY: misc_feature
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Matches 1078; Conserv
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                                                239 CGCATGGCCAAGGAGTGTGGGCGTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC
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                                                                                                                                                                                                                                                                                                                                                        Sequence 1035, Application US/1011722
; Bublication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmang, Jie
APPLICANT: Drmang, Jie
; TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 104C1P2BC1P
; CURRENT APPLICATION NUMBER: US/10/117,722
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SEQ ID NO 1035
; LENGTH: 1230
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99.8%; Pred. No. 0;
iive 0; Mismatches
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Best Local Similarity 99.8
Matches 1078; Conservative
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; NAME/KEY: CDS
; LOCATION: (119)..(1198)
US-10-117-722-1035
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ORGANISM: Homo sapiens
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US-10-117-722-1035
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                                                                                                                                                                                                                                                                       Score 1076.8;
Pred. No. 0;
0; Mismatches
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
FUNERTY FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SEQ ID NO 1035
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.8%;
Matches 1078; Conservative 0
                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(1198)
US-10-037-270-1035
                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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                                           CCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGATCTCCCAGTGGATGAG
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359 TACGGGGGGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG
                                                                           TICCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGGATCTGGAGACACTAATAATTTT
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(486)
OTHER INFORMATION: n = A,T,C or G
RESULT 8
US-09-918-995-5220
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                          Sequence 1514, Application US/09880107

Patent No. US20020142981A1

GENERAL INRORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14
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                                                                                                                                                                                                                                                               ; OTHER INFORMATION; Genbank Accession No. US20020142981A1 AA621146
US-09-880-107-1514
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REPRENCE: 20141-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT APPLICATION NUMBER: US/09/215,076

PRIOR PILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FSSESEQ for Windows Version 3.0

SEQ ID NO 5220

LENGTH: 486
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                                                                                                                                                                                                                                                                                                                                                 Query Match 38.7%; Score 418; DB 9; I
Best Local Similarity 98.6%; Pred. No. 4.9e-124;
Matches 432; Conservative 0; Mismatches 5;
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1514
LENGTH: 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1063 AAAAAATCAAGTCTTAA 1080
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990 AGTGGGCAAGAAGGTCCTGGTCACTGTTGAAGAGGATGACACCATCATGGAAGAATTGGT 1049
210 GCATGGCCAAGGAGTGTGGGGCTGATTGTGCTAAGTTCCAGAAGAGTGAGCTAGAATTCA 269
                                                                                                                                            169 GCTGGGCAAGTCTGTGGTGGCCAAAGTGAAAATTCCGGAAGGCACCATTCTAACAATGGA 228
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                                                                                                                     242 ACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGGT
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                                                                                                                                                                                                                          390 ACGCCGAGGAGGCTGGGATCTTCTTCACTGCCTCTGGCATGGATGAGA 437
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1050 AGATAATCATGGCAAAAAAATCAAGTCTTAA 1080
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 25343
LENGTH: 417
                                                                                                                                                                                                                                                                                                  RESULT 10

'0.09-918-995-25343

'Sequence 25343, Application US/09918995

'Publication No. US20030073623A1

'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-00-918-995-19353
; Sequence 19353, Application US/09918995
; Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(417)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-25343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                     291 AAGTTTAATCGGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                      61 ATCATTGCCGAGATCGGCCAGAACCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATC
                                                                                                                                                                                                   AAGITITAATCGGAAAGCCTTGGAGGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                   TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG
                                                                                            1 ATGCCGCTGGAGCTGTGTCCCGGGCGCTGGGTGGGCGGCGAAACACCCGTGCTTC
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                                                            Gaps
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              34.4%; Score 371.8; DB 10; Length 486; 99.5%; Pred. No. 4.3e-109; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.2%; Score 336.8; DB 10; Length 442; Best Local Similarity 98.0%; Pred. No. 8.5e-98; Matches 341; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATE Hyseq, inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERRACE: 20411-756
CURRENT APPLICATION NUMBER: US/09/218,995
CURRENT FILING DATE: 2001-07-30
FRIOR PELLOATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PASLESEQ for Windows Version 3.0
SEQ ID NO 28620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-918-995-28620
; Sequence 28620, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)...(442)
; CTHER INFORMATION: n = A,T,C or G
US-09-918-995-28620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 TTCCTGCATGAACTG 485
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                                 Best_Local Similarity 99.5
Matches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AGTGGGCAAGAAGGTCCTGGTCACTGTTGAAGAGGATGACACCATCATGGAAGAACTGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GCGTGCCCTGGGCTCCCCAACCAAGCTGCTGCTGTGAGATGGCCTGCAATGAGAA 170
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Sublication No. US20030180738A1

GENERAL INFORMATION:

APPLICANT: The No. US20030180738A1tingham Trent University

TITLE OF INVENTION: Cancer Associated Genes and their Products

FILE REFERENCE: No. US20030180738A1tingham Trent Uni

CURRENT APPLICATION NUMBER: US/10/181,447A

CURRENT FILING DATE: 2002-07-18

PRIOR FILING DATE: 2001-01-18

PRIOR FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 18

LENGTH: 404
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 480;
             APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT PILLING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/215,076
FRIOR APPLICATION NUMBER: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 19353
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                Score 315.8; DB 10;
Pred. No. 5.4e-91;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 AGATAATCATGGCAAAAAA 1068
                                                                                                                                                                                                                                                                                                  // NAME/KEY: misc_feature
// LOCATION: (1)...(480)
// CTHER INFORMATION: n = A,T,C or G
US-08-918-995-19363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AGATAATCATGGCAAAAA 369
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.2%;
Best Local Similarity 99.4%;
Matches 317; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(404)
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-181-447A-18
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us-10-11 13

us-10-106-698-2649

isequence 2649, Application US/10106698

isequence 2649, Application US/10106698

isequence 2649, Application US/10106698

isequence 2649, Application No. US20030109690A1

isequence 2649, Application No. US20030109690A1

isequence 2649, Application No. US20030109690A1

isequence 2649, Application No. US20030A1

isequence 2649, Application No. US20040A1

isequence 2649, Application No. US20040A1

isequence 2649, Application No. US20040A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTTTAATCGGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AAGTITAATCGGAAAGCCTTGGACAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG 343
                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                     104 ATGCCGCTGGAGCTGTGTCTCCCGGCCCTGGTGGCTGCCCGCAACACCCCGTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 ATCATTGNCGAGATCGGCCAGAACCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ATCATTGCCGAGATCGGCCAGAACCACCAGGCGACCTGGACGTAGCCCAAGCGCATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCCAGAAGAGTGAGCTAGAATTC
                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                             Score 280.6; DB 15; Length 404; Pred. No. 1.2e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTCAGGG 391
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or c
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LOCATION: (287). (287)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (300). (300)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (370). (370)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (374). (374)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (402). (402)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (405). (405)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (405). (405)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (405). (406)
; OTHER INFORMATION: n = g, a, t, or US-10-181-447A-18
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                                                                                                                                  26.0%;
                                                                                                                                                                            Best Local Similarity 98.3
Matches 283, Conservative
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APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2065
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
FROM IN 03132
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Pred. No. 1.9e-47;
0; Mismatches 3; Indels 0;
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                                                                                                                                                                US-10-242-535A-31232
; Sequence 31232, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
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; LOCATION: (31)...(31)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-31232
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Best Local Similarity 98.4%;
Matches 181; Conservative
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ORGANISM: Human
PRATURE:
NAME/KEY: misc_feature
LOCATION: (6)..(6)
OTHER INFORMATION: n is a, c
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Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Chondrodene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-8

PRIOR FILING DATE: 2001-03-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SEQ ID NO 31232

LENGTH: 203
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0; Mismatches 6; Indels 2;
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Matches 181; Conservative 0; Mismatches 3; Indels 0;
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Dikaryogis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1080).
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Homo sapiens NANS gene, VIRTUAL TRANSCRIPT, partial sequence,
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GSS 17-DEC-2003

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Divaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bulkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases I to 984)

E 1 (bases I to 984)

E 1 (bases I to 984)

E 11, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

U mpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12942945.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5047.f For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODK004BE07NP1&cluster=5047.f. Contact:

Feng Liang Bmail: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ Invitrogen com/ Invitrom/ Invitrom/
                                                                                                                                                                                                                                                                                                                                                                                                                EST 01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" / note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecox sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                            AL578658 Anno sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK004X114 3-PRIME, mRNA sequence.
                           1021 GAGGATGACACCATCATGGAAGATTGGTAGATAATCATGGCAAAAAAATCAAGGTCTTAA
                                                                                                        GCCTATCCTCCTGAAGACATCTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTGTTGAA
                                                                                                                                                                                                                                961 GCCTATCCTCCTGAAGACATCTTTAATCTAGTGGGCAAGAAGGTCCTGGTCACTTGAA
                                                                                                                                                                                                                                                                        1021 GAGGATGACACCATCATGGAAGAATTGGTAGATAATCATGGCAAAAAATCAAGTCTTAA
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/cell type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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Pred. No. 5.7e-236;
3; Mismatches 12;
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/db_xref="taxon:9606"
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                Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive
                                                                                                                                                                                                                                                                                        29; Length 1080;
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Pred. No. 3.4e-268;
0; Mismatches 2;
                                                                                                1. .1080
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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/gene="NANS"
/locus_tag="HCM5357"
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Best Local Similarity 99.8%;
Matches 1078; Conservative
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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 31006 EVRY cedex - France
BP 191 31006 EVRY cedex - France
Email: seqrefegenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5047.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL001BD11NP1&cluster=5047.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODL001BD11NP1.
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/db_xref="taxon:9606"
/cb_lrype="C$DL01XG22"
/cell type="R CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cellihne="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)
25-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR viets of the pcMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCATGGCCAAGGAGTGTG-GGCTGATTGTGCTAAGTTCCAGAAGAGTGAGCTAGAATTC
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Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 1201)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDMA libraries and normalization
Unpublished (2001)
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Pred. No. 3.8e-235;
.; Mismatches 10; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                 864 GAAGCAITCCTGGGGGAAGACGTACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGA
                                                                                                                                 CCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGGATCTTCTTCACTGCTCTGG
                                                                                                                                                                                                                   CATGGATGAGATGGCAGTTGAATTCCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGG
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                        GAAGCATTCCTGGGGGAAGACGTACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGA
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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                 Score 917.8; DB 9;
Pred. No. 6.2e-227;
8; Mismatches 23;
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Best Local Similarity 96.6%;
Matches 958; Conservative
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BP 191 91006 ENRY cedex - France
Email: sequelegenoscope.ons.fr. Web: www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5047.f For
more information about this cluster, see
http://www.genoscope.ons.fr.
cgi-bin/cluster.cgifseq=CSODK001BG11NP1&cluster=5047.f. Contact :
Ferg Library Enis filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK001BG11NP1.
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1 (Doases 1 to 990)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001)
Contact: Genoscope
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TTCTTGCAGTGTACCAGCGCATACCCGCTCCAGCCTGAGGACGTCAACCTGCGGGTCATC
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                       TTCTTGCAGTGTACCAGCGCATACCCGCTCCAGCCTGAGGACGTCAA-CTGCGGGTCATC
                                                               TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCCATGAAACAGGC
                                                                                   TCGGAATATCAGAAGCTCTTYCCTGACATTCCCATAGGGTATTCTGGGCATGAMACAGGC
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/mol_type="mRNa"
/db_xref="taxon:9606"
/clone="CSODKONYM22"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
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Clark.A.G.; Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TATGGGGAGCACAAGCGGCATCTGGAATTCAGCCACGACCAGTACAAGGAGCTGCAGAGC 300
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     33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitsion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Fockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
92 ATTCCGGAAGGCACCATTCTMACAATGAACATGCTCACCGTGAAGGTGGGGTGAGCGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTTTAATCGGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AAGTTTAACCGGAAGGCCCTGGAGACCATATACTTCGAAGCATTCATGGGGGAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCATCGCGGAGATCGGCCAGAACCACCAAGGAGAATAGATGTGGCCAAGCGCATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CGCACTGCCAAGGAGTGTGGGGCCGACTGCGCTAAGTTTCAGAAGAGCGAGTTGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                Mus musculus NANS gene, VIRTUAL TRANSCRIPT, partial sequence, AX414839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 883.2; DB 29; Length 1080;
Pred. No. 6.3e-218;
0; Mismatches 123; Indels 0;
                                960 AGCCTATCCTCGAAGACATCTTTAATCTAG 991
                                                   AGGCTATCCTCCTGAAGACATCTTTAATCTAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1080
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="NANS"
/locus_tag="HCM5357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                        AY414839.1 GI:39770798
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Best Local Similarity 88.6%;
Matches 957; Conservative 0
                                                                                                                                                                                                                                                                          Mus musculus
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JOURNAL
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AY414839
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PUBMED AUTHORS

REFERENCE

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/ DOCUMENT 1 de "BAC36290.1"

/ DECHEID 1 de "BAC36290.1"

/ DE XTEF = "GI:26345280"

/ AD XTEF = "GI:2634580"

/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGCCGAGGAGGTTGGGATCTTCTTCACTGCCTCTGGCATGGATGAGATGGCAGTTGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGCGCAGGAGATCGGCATCTTCACTGCCTCTGGCATGGACGAGATGGCAGTTGAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITCIGCACGAACIGAAIGIICCCTITIICAAAGIIGGAACIIGGGGGACACIAACAAIIII 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCGCCATATCTGTGGCCGCGCGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACG 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGGACAAGACCIGGAAGGGGGAGIGACCACICGGCCICGCIGGAGCCIGGAGAACIGGCC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAATGGGACACCATGAAGCAAGTCTATCAGATCGTGAAGCCGCTGAATCCCAACTTCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
       (MGD MGI:2149820, GB NM 053179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 883.2; DB 11; Length 1906;
Pred. No. 8.5e-218;
0; Mismatches 123; Indels 0;
       sialic acid synthase (MGD|MGI:21498:
evidence: BLASTN, 100%, match=1140)
                                                                              /codon_start=1
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32. _1111
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome_Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Pumamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramateu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S Adachi, J. Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, P., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Itoh, M., Izawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, H., Sato, R., Sakai, K., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshido, M., Muramatsu, M., and Hayashizaki, Y., Direct, Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1906)
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Fax:81-45-503-9216)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
1. .1906
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/clone_libe="NIH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon, kidney, stomach; Vector:
pcwv-spoRrf; Site_l: Not!, Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invircogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1404 row. k column: 21
High quality sequence stop: 856.
High quality sequence stop: 856.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
   TCGGAATACCAGAAGCTCTTTCCCCGACATTCCCATCGGGTATTCCGGGCACGAGGC
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                                                             TICCTGCATGAACTGAATGTICCATTTTTCAAAGTTGGATCTGGAGACACTAATAATTTT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Bmail: sequenceope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5047.f For
nore information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODK004BE07QPl&cluster=5047.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK004BE07QPl.
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AL556387 Homo sapiens HELA CELLS COT 25-NORWALIZED Homo sapiens CDNA clone CSODKO04YI14 5-PRIME, mRNA sequence.
AAGACCTGGAAGGGAGTGACCACTCGGCCTCGCTGGAGCCTGGAGAACTGGCCGAGCTG
                                          GAAGGCACCATTCT-AACAATGGACATGCTCACCGTGAAGGTGGGTGAGCCCAAAGCCTA
                                                                                                                                                      GAAGGCACCATTCTAAACAATGGACATGCTCACCGTGAAGGTGAGCCCAAAGGCTA
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Law, B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12899016.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12789734.

Contact: Genoscope
Contract: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Invitrogen. This sequence belongs to sequence cluster 5047.f For more information about this cluster, see

Invitrogen. This sequence belongs to sequence cluster 5047.f For more information about this cluster, see

http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODC016BG11NP1&cluster=5047.f. Contact :
Freng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODC016BG11NP1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                            TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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E 1 (bases 1 to 889)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (Inc.

CDNA Library Preparation: Life Technologies (Inc.

CDNA Library Preparation: Life Technologies (Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/Linl at:

http://image.llni.gov

Plate: LLAM13470 row: d column: 19

High quality sequence stop: 724.
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                                           CCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGTCTGTGGTGGCCCAAAGTGAAAATTC
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Pred. No. 1.9e-202;
0; Mismatches 7; Indels 1;
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Best Local Similarity 99.1%;
Matches 838; Conservative
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Homo sapiens
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us-10-759-277-3.rst

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/tissue_type="lymphoma, cell line"
/lab_host="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 99"
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G) size-selected >Slobp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                         AGENCOURT 6853542 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5926258 5', mRNA sequence.
       657 TCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGTATTCTGGGCATGAAACAGGC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2099 row: e column: 11
High quality sequence start: 22
High quality sequence start: 22
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1031)

                                                                                                                       721 TTGGACAAGACCTGGAAGGGGAGTGACCACTCGGCTCGCTGGAGGCCTGGAGAACTGGCC
                                             661 ATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACT
                                                                               717 ATAGGGATATCTGTGGCCGCAGTGGCTCTGGGGGCCCAGGTGTTGGAACGTCACATAACT
                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 GGAGTTCAGCCATGACCAGACAGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 GGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGATCTT
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                                                                                                                                                                                                 781 GAGCTGGTGCGTCAGTGCGTCTTGTGGAGCGTGCC 816
                                                                                                                                                                                                                     73.7%; Score 796.4; DB 13;
99.1%; Pred. No. 2.1e-195;
live 0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5926258"
                                                                                                                                                                                                                                                                                                                                                                                                                BQ064521.1 GI:19893231
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                         /tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/close lib="NIH MGC 72"
/note="Organ: skin; Vector: pCNV-SPORT6; Site 1: Not1;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TACGGGGGGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 TACGGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGAGCTGCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCCGCTGGAGCTGGAGCTGTCCCGGGCGCTGGGTGGGCGGGGAACACCCGGTGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.4%; Score 803.2; DB 13
99.0%; Pred. No. 3.3e-197;
tive 0; Mismatches 8;
               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                       High quality sequence stop: 711.
Location/Qualifiers
                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6167793"
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Matches 808; Conservative
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CITCACTGCCTCTGGCATGGATGGCAGTTGAATTCCTGCATGAACTGAATGTTCC 142
                     443
                                                                                                        504 TTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGCTTCTTGCAGTGTACCAGGGCATA
263 TTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGCTTCTTGCAGTGTACCAGGGCATA
                                                                                                                                                                                                                                                     GGCTCTGGGGGCCCAAGGTGTTGGAACGTCACATAACTTTGGACAAGACCTGGAAGGGGAG
                                                                                                                                                                                                                                                                                                                                      563 TGTGGAGCGTGCCCTGGGCTCCCCAACCAAGCAGCTGCTGCCCTGTGAGATGGCCTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                AAAAGGTCGCCCAATGGTCATCTCCAGTGGGATGCAGTCAATGGACACCATGAAGCAAGT
                                                                         203 AAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAGTCAATGGACACCATGAAGT
                                                                                                                                                   564 CCCGCTCCAGCCTGAGGACGTCAGCGGGTCATCTCGGAATATCAGAAGCTCTTTCC
                                                                                                                                                               GGCTCTGGGGGCCAAGGTGTGGAACGTCACATAACTTTGGACAAGACCTGGAAGGGGAG
                    ATTITICAAAGITIGGATCIGGAGACACIAAIAATTITCCITAICIGGAAAGACAGCAGAAA
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